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Wildlife protection and biodiversity conservation - A review on utility of forensic DNA analysis

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ABSTRACT

The utilization of DNA examination in forensic cases concerning animal maltreatment and biodiversity preservation is presently increasing. Violations, for example, unlawful gathering/carrying, poaching, and illicit exchange of ensured species are progressively being researched utilizing DNA-based confirmation in numerous nations. Utilizing DNA investigation, it is conceivable to distinguish the species and geographical emergence (i.e. populace) of a forensic specimen and to likewise individualize the specimen with

maximum likelihood. Notwithstanding broad writing in animal species, there is tragically a genuine absence of data on plant species, with just a modest bunch of late reviews. In the present study, a differing scientific examination and detailed application that have been completed to date while additionally highlighting late formative reviews which offer a scientific potential for numerous species later on.

Keywords: DNA, species, forensic examination, wild life, identification

1. INTRODUCTION

Forensic DNA examination in examinations of violations, for example, animal mercilessness and poaching, and unlawful gathering and exchange of flora and fauna have seen quick development as of late essentially due technological propels made in the field of human legal genetics which has permitted the exchange of techniques and applications to various non-human species. In any case, the advance has been more gradual than with human forensic genetics qualities for various reasons. Firstly, not at all like human forensic qualities, legal DNA examination for animal security and biodiversity preservation needs to bargain with a plenty of species prompting to an absence of ideal genetic markers for some. Besides, animal/plant/wildlife life geneticists have for many years worked in detachment from criminological geneticists, resulting in markers and procedure without the broad validation procedures required for scientific casework. Thirdly, a much of the poaching and illicit gathering of normal assets happens in poor countries where budgetary assets are restricted (1). Lastly, animal/plant/wildlife wrongdoing dependably takes bring down need to crime involving people. Along these lines, except for a couple domesticated animal and plant species, there has been restricted contribution of resources into different species. More than 20,000 species are right now listed in the IUCN Red List of Threatened Species. The rundown encompasses diverse types of earthbound plants, for example, cycads and desert plants, in addition to vertebrates, for example, angle, creatures of land and water, reptiles, birds, and warm blooded animals, and spineless creatures, for example, lobsters, crabs, and corals (2). The use of scientific DNA investigation techniques in these species has clears potential.

2. KINDS OF BIOLOGICAL EVIDENCES

When exploring violations against animals or ensured natural resources, there is an excess of the sorts of tests that may be experienced. From the investigation of more standard samples such as tissue, hair, and quills, DNA examination has additionally been carried out utilizing tests, for example, tusks, hooks, tanned cowhide, bile crystals, scales, shells, prepared creature parts and subsidiaries inside Traditional Chinese Medicines (TCMs), and objects made out of animal parts, for example, hankos, shawls, idols and purses. Although a few cases including diverse animal species have been accounted for to date, there are detectably no announced scientific cases including plant species. A substantial number of formative reviews with great potential for forensic applications have been reported for by and by, fusing unordinary sorts of natural proof, and luckily, a couple are of plant species (1).

3. FORENSIC SIGNIFICANCE

Studies to date have detailed differing sorts of scientific investigations including poaching, unlawful trade, location of protected species inside TCMs, domesticated animals theft, and illicit smuggling of animals (Table 1 and Table 2). Not at all like in forensic genetics qualities where the predominant goal is the individualisation of a specimen (e.g. for establishing the match acquired between an evidentiary specimen and a presume specimen), when exploring crimes including secured vegetation or fauna, there is all the more regularly the requirement for species distinguishing proof than individual recognizable proof. In an expansion, there is much of the time the need to pinpoint the land district of the populace that specific samples started from.

Table1 Types of forensic investigations carried out to date

Species Name	Type of biological evidence	DNA marker	Type of investigation	Reference
Chinese water deer	Meat, Skin	Southern Blotting and Hybridisation	Species Identification (poaching)	3
India peafowl	Cooked meat,	mt DNA sequencing	Species identification	4

	intestine, dried tissue from chopping board	(cytb, 472 bp)	(poaching)	
Chinese Silka deer subspecies	Skin, Blood	mt DNA sequencing (CR, 1079bp)	Sub-species identification (poaching)	5
Wild boar	Blood stains from Knife, carcass	STRs	Individual identification (poaching, animal cruelty)	6
Great White Shark	Tissues from dried fins	Nuclear ribosomal ITS2, 560 bp; 511bp	Species Identification (illegal trade)	7
Roe deer	Meat, Hair	Mt DNA sequencing (cyt b, 900bp)	Species identification (poaching)	8
Pheasant	Meat	Sexing (CHD-1, 230-280bp)	Sex identification (poaching)	8
African Elephants	Tusks	STRs	Determination of geographical origin of seized ivory (illegal trade)	9
African Elephants	Hankos	STRs	Determination of geographical origin of seized ivory (illegal trade)	10
Tiger	Traditional East Asian Medicine	mt DNA species-specific amplification (cyt b)	Species identification (identification in traditional east Asian medicine)	11
Beaked Whale (Mesoplodon ginkgodens)	Solid Tissue	mt DNA sequencing (CR 363 bp)	Species identification (contravention of CITES and US Marine Mammal Protection Act)	12
Asiatic black bear	Bile Crystals	mt DNA sequencing (cyt b, 175bp)	Species identification in traditional East Asian medicine)	13
Several mammal species	Solid tissue, swabs, clothing, blood stained carpet	mt DNA sequencing (CR 503 bp)	Species identification (mixed forensic samples)	14
Guanaco	Meat	mt DNA sequencing (cyt b, 774bp), STRs	Species and individual identification (poaching)	15
Northern European Brown Bear	Hair, Blood stain	STRs	Individual identification (illegal hunting)	16
Meat (Sashini)	mt DNA sequencing (cyt b, 400bp)	Species identification (illegal trade)	Whale Species	17
Commercial fish products in Italy	mt DNA sequencing (cyt b, 300 bp, COI,	Species identification (food traceability/	Muscle	18

	600 bp)	illegal trade)		
Crocodile	mt DNA sequencing (COI, 645 bp)	Species identification	Crocodile Skin Handbag	19
Chimpanzees	STRs, Population assignment tests	Determination of geographical origin (illegal animal smuggling/ hunting)	Blood	20
Wolf	STRs	Individual identification (illegal killing)	Teeth	21
Tiger	mt DNA sequencing (CR), STRs	Individual identification (illegal killing)	Claw and decomposed skin	22
Sardinian mouflon	STRs	Individual identification (poaching)	Blood stains from scene of crime, carcass	23
Parrots and Cockatoos	mt DNA sequencing (12S, 230 bp, Cyt b, 500bp)	Species identification (illegal smuggling)	Embryonic tissue	24
Reed Buck	mt DNA sequencing (COI, 650 bp)	Species identification (poaching)	Meat, Carcass	25
Wildebeest	STR	Population assignment of sarcoptes mites (illegal trade while infected)	Mites	26
South American Camelids	STRs (mt DNA sequencing not useful due to past hybridisation events)	Species identification (illegal smuggling)	Blood	27
Moose	STRs	Determination of geographical origin (illegal hunting)	Solid tissue	28
Lowland tapir	mt DNA sequencing (cyt b, 1070 bp)	Species identification (poaching)	Meat	29
Asiatic Black bear, suspected felid	mt DNA sequencing (COI, 708 bp, CR-279-744 bp, cyt b, 554 bp)	Species identification	Hair, tanned leather	30
Fox	STRs	Individual identification	Blood, Solid Tissue	31
Indo-China spitting Cobra	mt DNA sequencing	Species identification (illegal trade)	Tissue from snake wine	32
White tailed black cockatoos	STRs	Individual identification (poaching, illegal collection/ killing)	Feathers	33
Cyprit mouflon	mt DNA sequencing (cyt b, 1140 bp), STR	Individual identification (poaching)	Blood stains from suspects boot & jeans, carcass	34
Scarlet macaw	mt DNA sequencing (COI, 648 bp), one STR locus, sexing (CHD-1)	Species identification (illegal trade)	Feathers	35

Sturgeons and Paddlefish	mtDNA sequencing (cyt b, 850 bp; CR, 725 bp)	Species identification (mislabelling/illegal trade)	Caviar	36
Wolves or dogs	STRs	Individual identification (livestock depredation/false declarations)	Saliva samples from carcasses	37
Elephant	mtDNA sequencing (cyt b, 357 bp; CR, 377–630 bp)	Species identification and determination of geographical origin (illegal trade)	Ivory seals	38
Southeast Asian monitor lizards	mtDNA sequencing (ND1, 1181 bp)		Muscle, liver, skin, scale clippings	39

Table 2 Developmental studies with forensic application

Animal / Plant Species	Type of Evidence	DNA marker	Forensic application	References
Animal Species				
Rhinoceros	Horn	mt DNA sequencing (cyt b, 402 bp)	Species identification (illegal trade)	40
Tiger	Blood	STRs	Individual identification and estimation of numbers	41
Chinese alligator	Meat/Skin	mt DNA sequencing (cyt b, 180 bp)	Species identification (illegal hunting/ trade)	42
Various shark species from the Hong Kong shark fin market	Fin	DNA sequencing (Nuclear ribosomal internal transcribed spacer2 or ITS2 (1282-1365 bp)	Species identification (illegal trade)	43
Tibetan antelope	Shahtoosh Shawls	mt DNA sequencing (cyt b, 311 bp)	Species identification (identification of Tibetan antelope wool)	44
Various whale species	Skin, blubber, meat	mt DNA sequencing (CR, 464bp), STRs	Estimation of numbers entering whale meat markets	45
Mule Deer	Solid Tissue	STRs	Development of STR	46

			profiling system (illegal killing)	
Seahorses	Tail tissue	mt DNA sequencing (cyt b, 696bp; CR 533 bp)	Species identification (illegal trade) and determination of geographical origin	47
Red Deer	Hair, Blood and other tissues	STRs	Individual identifications (poaching)	48
Various turtle species	Shells and fragments stir fried in vinegar	mt DNA sequencing (Cyt b, 340 bp)	Species identification (illegal trade)	49
Three Indian crocodile	Blood, Solid tissue, unknown hide	Species specific multiplex PCR (Cyt b, 373- 578 bp)	Species identification (illegal trade)	50
Plants Species				
Divergent angiosperm taxa	Leaves	Plastid DNA sequencing (trnA-psb A intergenic Spacer)	Species identification (develop barcode database)	51
Ramin Gonystylus spp.)	Leaves, wood, processed wood	SNP genotyping (matK gene)	Species identification (illegal trade)	52
Tropical timber (Neobalanocarpus heimii)	Inner bark leaves	Chloroplast DNA sequencing (trn L intron 584bp; trnG intron 660bp; trnK intron 569bp; psbK-trnS spacer 679 bp)	Determination of geographical origin within peninsular Malaysia (illegal harvesting)	53
Tropical timber (Neobalanocarpus heimii)	Inner bark leaves	STRs	Determination of geographical origin within peninsular Malaysia (illegal harvesting)	54
Agarwood (Aquilaria and Gyrinops spp.)	Leaves, wood, incense sticks	STRs	Determination of geographical origin (illegal harvesting)	55
Sapelli timber	Cambium, timber	STRs	Determination of geographical origin (illegal logging)	56

4. IDENTIFICATION OF SPECIES

In wildlife cases, species recognizable proof reason morphological perceptions may a few circumstances be conceivable to use, as a rule, the utilization of DNA-based techniques is the main alternative e.g. when attempting to set up the presence or absence of biological material from endangered species in inside prepared items. Mitochondrial control region or D-loop sequences (12, 14, 22, 5), gene sequences of ND1 (NADH dehydrogenase subunit 1) (39, 50) and sequences of ribosomal internal transcribed spacer (ITS-2) (7, 43, 52, 57) are used for species identification in animals. In any case, this has most usually been adept by sequencing the

cytochrome b (cyt b) or cytochrome oxidase subunit 1 (COI) region of mitochondrial DNA (mtDNA). Both the GenBank (www.ncbi.nlm.nih.gov/genbank/) and European Molecular Biology Laboratory (EMBL) (www.ebi.ac.uk/embl/) databases hold substantial numbers of these sequences. In 2003, further to a point of interest paper by Hebert et al. (2003) proposing the 5_ area of the COI quality (648 bp) as a potential widespread "barcode" for all creatures, a worldwide exertion called the Consortium for the Barcode Of life (CBOL) was set up (58). Overall sequencing endeavours have as of now brought about >2.4 million standardized tag records from differing species in its database – the Barcode of Life Data frameworks (BOLD) (www.boldsystems.org/). Not at all like community databases, for example, EMBL and GenBank, BOLD has a quality control framework worked in, and before a scanner tag is acknowledged, certain data is obligatory. For example, points of interest are required on the specimen (e.g. accumulation date and area with GPS facilitates), a voucher example (e.g. list number and organization), and the PCR primers utilized. Additionally, sub-mission of the first original documents is required (58). All inclusive PCR primers have been utilized crosswise over significant gatherings e.g. Hebert et al. (2004) (59) and Ivanova et al. (2007) (60) have announced universal primers that can amplify up 5' region of the COI sequence in 260 and 94 species of birds and fish respectively; Naro-Maciel et al. (2010) (61), Bitanyi et al. (2011) (62) and Clare et al. (2011) (63) used COI primers for identification in across 20 species of antelopes, 163 species of neotropical bats and 7 species of marine turtles, respectively.

Hebert et al. (2004) (59) study in on North American winged animals uncovered that normal Kimura-2 parameter (K2P) gap evaluation were 7.93% and 0.43% between and inside species, separately. Additionally, Naro-Maciel et al. (2010) (61) revealed <0.9% intra-particular variety be that as it may, >1.68% between particular variety, making a valuable "bar coding crevice" for the recognizable proof of species. Therefore, gave a few data on the levels of between and intra-particular variety is accessible, COI bar coding seems to offer scientific researchers the likelihood of contrasting a succession produced from a measurable specimen to existing arrangements inside the database to accomplish fruitful species recognizable proof. Be that as it may, COI bar coding has gone under broad feedback as of late regarding its apparent legal potential. For instance, it has been over and again recommended that given mtDNA has been appeared to display broad heterogeneity in rates of advancement, species depiction utilizing separation measure edges is flawed (e.g. Galtier et al. 2009 (64); Vences et al. 2005 (65)). Also, K2P gap evaluations broadly utilized as a part of DNA bar coding for the basic reason that they were utilized as a part of the first paper by Hebert et al. (2003) (66), are viewed as improper, particularly at the point when species are firmly related (Srivathsan & Meier 2012) (67). There have likewise been reports on the absence of vigour of general bar coding ground works depicted in writing and a genuine absence of satisfactory ordered scope of a few gatherings of creatures inside BOLD (e.g. 68, 69,70,71). Utilizing a determination of presented and endemic Australian well evolved creatures, Wilson-Wilde et al.(2010) found that there was an extensive absence of arrangements from Australian local species which brought about bizarre species distinguishing proof after COI sequencing and phylogenetic investigations in various cases. Boykin et al. (2012) (68) taking a glance at 88 types of obtrusive bugs and looking at GenBank and BOLD databases in terms of their utility for species depiction, found that there were numerous a bigger number of arrangements in GenBank than there were in BOLD. In plants, the COI quality is in reality now considered a poor decision for species recognizable proof as a result of low rates of substitution, and the CBOL plant working gathering has proposed the utilization of a centre arrangement of two coding groupings from plastids (rbcL and matK), with conceivable extra markers, for example, plastid intergenic spacer trnH-psbA and atomic inside deciphered spacer of ribosomal DNA (nrITS) (72). These are in this way, the districts that have been focused in the few reviews on plant species to date (51-53). Moreover, unwavering quality of species ID utilizing COI bar coding has been observed to be fundamentally lessened in heteroplasmic species and when co-amplification of nuclear mitochondrial DNA segment is an issue. Heteroplasmy, albeit inadequately considered in many species, has been all around reported in people and a few spineless creatures. In Hawaiian Hylaeus honey bees, Magnacca and Brown (2010) (73) watched that heteroplasmic species demonstrated hard to distinguish utilizing COI bar coding, notwithstanding when capable Bayesian phylogenetic techniques were utilized. The nearness of nuclear mitochondrial DNA segments in a few plants and also invertebrate and vertebrate creatures has been very much recorded (73-76). The test postured by the co-amplification of numts to species distinguishing proof utilizing COI barcoding in the bug arrange Orthoptera was researched by Moulton et al. (2010) (75). Their outcomes recommended that numts were across the board in these bugs and were promptly coamplified utilizing general preliminaries. Albeit expanding preliminary specificity helped at times, it neglected to totally dispose of numt co-amplification. In a few animal types due to past hybridisation occasions, mtDNA sequencing utilizing COI is not instructive for separating species additionally, different techniques are required. For instance, when both cyt b also, COI sequencing demonstrated uncertain, Di Rocco et al. (2011) (27) in an examination concerning illicit carrying of alpacas from Bolivia to Argentina expected to utilize Short Tandem Repeat (STR) genotyping taken after by populace task to affirm that creatures seized from an agriculturist were alpacas or alpaca half and halves as opposed to immaculate llamas. At long last,

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Taylor and Harris (2012) (70) raise doubt about the whole eventual fate of DNA bar coding given Next Generation Sequencing (NGS) advances where whole genomes are turning out to be anything but difficult to grouping generally modestly. They suggest that NGS advances would conquer various issues, for example, the nearness of heteroplasmy and numts, and the dependence on a solitary quality which has been over and over censured (77). In spite of the numerous reactions confronted by DNA bar coding anyway, it keeps on being generally utilized for the motivation behind species recognizable proof.

5. IDENTIFICATION OF INDIVIDUALITY

Individual identification, most generally accomplished utilizing STR profiling, might be required for instance, when a DNA match is being examined between an illicit murder (e.g. body/remains) and proof gotten from a poacher (e.g. skin/meat). On the off chance that there is a match between the DNA profiles created, the likelihood of a match (additionally called the maximum match likelihood or RMP) can be ascertained given appropriate allele recurrence databases are accessible. Nonetheless, dissimilar to trained species, for example, mutts and felines, when one considers the quantity of untamed life species required, there are still not very many allele recurrence databases. Illustrations incorporate Wasser et al. (2004) (78) in African elephants (n = 399); Dawnay et al. (2008, 2009) (79,80) in badgers and fowls of prey in the UK (n = 14–190), Jobin et al. (2008) (46) in mule deer in Alberta (n = 117–129), Eiken et al. (2009) (16) in Norwegian chestnut bears (n = 232); Caratti et al. (2010) (81) in wild pigs in North West Italy (n = 142), Gupta, Bhagavatula, et al. (2011) (22) in tigers in India (n = 34), Lorenzini et al. (2011) (23) in Sardinian mouflon (n = 58); White et al. (2012) (33) in Australian red followed dark cockatoos (n = 30) and Harper et al. (2013) (82) in southern white and dark rhinoceros (n = 367 and 33 separately). In spite of the fact that at least 500 people is prescribed for solid allele recurrence gauges in human population genetics (Schneider 2007) (83), sourcing such huge numbers is a troublesome errand in protected endangered species since they are by definition uncommon, in little numbers, and requiring broad printed material for trade of tests because of CITES (Convention on International Exchange Endangered Species of Wild Fauna and Flora) directions. Moreover, examining will rely on upon the home range, spatial conduct, also, conceptive system of the species concerned. Evaluations of F_{ST} which are fused routinely inside calculations of RMPs in people to amend for the improved probability of seeing a similar DNA profile in various people when they have a place with an indistinguishable subpopulation from a consequence of co-lineage than when they have a place with various subpopulations have likewise been detailed in non-human creature species. Values go from 0.02 in mule deer in Alberta by Jobin et al. (2008) (46), 0.046 in wild pig from North West Italy via Caratti et al. (2010) (81), 0.09 in Northern European brown bears by Andreassen et al. (2012) (84), 0.1 in Norwegian brown bears by Eiken et al. (2009) (16), up to 0.12 in UK badgers by Dawnay et al. (2008) (79). Consolidation of F_{ST} evaluates inside RMP computations for non-human species is in actuality especially critical since F_{ST} qualities are frequently far higher in untamed life species where populace substructure has a tendency to be high (evaluations from >1000 types of plants and creatures demonstrate a wide range, with values ordinarily around 0.1–0.2) (Barton et al. 2007) (85). In people in differentiate, F_{ST} qualities are 0.03 at the exceptionally most extreme (Budowle et al. 2001) (86). Addition to this, it is viewed as critical to amend for inbreeding inside a subpopulation by fusing values for the inbreeding coefficient FIS (or f) inside RMP calculations. In doing as such, the RMP is adequately expanded at homozygous loci. This is huge since when inbreeding inside a populace is high, the probability of watching homozygous genotypes increments inside people (Ayres and Overall, 1999) (87). Despite the fact that redress for inbreeding is not utilized as a part of human DNA profiling because of to a great degree low levels of inbreeding (with not very many special cases), it is profoundly important in debilitated species that have encountered exceptional decreases in numbers and exist in divided, intermittent territories. F_{IS} gauges have likewise been accounted for in a few reviews e.g. 0.005 in Northern European brown bears (Andreassen et al. 2012) (84), 0.089 in wild pig from North West Italy via Caratti et al. (2010) (81), 0.11 in UK badgers (79).

A gauge like the RMP however not identifying with a specific legal profile, regularly utilized as a part of untamed life contemplates on the grounds that it likewise mirrors the level of hereditary differences is known as the Probability of Identity $P_{(ID)}$ (Waits et al. 2001). By considering all people inside a populace to be full-sibs, one can acquire the $P_{(ID)sib}$, an exceedingly preservationist upper bound Probability of Identity, which is valuable in a criminological setting (88). Both $P_{(ID)}$ furthermore, $P_{(ID)sib}$ gauges have subsequently been accounted for in a number of species e.g. Lorenzini et al. (2011) (23) in Sardinian mouflon, Andreassen et al. (2012) (84) in Northern European cocoa bears, White et al. 2012 (33) in cockatoos, with qualities running from 2.6×10^{-20} to 4.6×10^{-8} and 2.4×10^{-8} to 1.3×10^{-4} for $P_{(ID)}$ and $P_{(ID)sib}$ separately. There are many reports of individualisation utilizing STRs and the forensic examinations have been extremely different. They incorporate animal savagery (6), poaching (15, 23, 34- 33), illicit chasing/ slaughtering (16, 22, 37) and illicit discharge (89) – see Table 1 and segments beneath for subtle elements.

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6. DETERMINATION OF GEOGRAPHIC ORIGIN

It is regularly critical in scientific science to likewise attempt and decide the populace from which a specific example was inferred i.e. do populace assignment. MtDNA sequencing and phylogeographical investigations have been utilized for deciding the topographical source of an example e.g. Sanders et al. (2008) (47) allocated seahorses purchased from shops in San Francisco and focal California to their land inception from over the world utilizing D-loop successions, and Lee et al. (2013) (38) additionally utilized D-loop arrangements to set up whether ivory seals seized by police in South Korea were from African savannah, African woodland or Asian elephants. Despite the fact that D-circle sequencing is much of the time utilized for tests with a broad hereditary structure as in the cases above, more fine scale populace assignment is normally accomplished utilizing STR genotypes. Utilizing assignment tests, individual multi locus STR genotypes can be appointed to populaces (groups of people) based on allele frequencies and the probability of an individual's genotype having a place with that populace contrasted with alternate populaces. Subsequently, an individual, if rejected from everything except one populace will be relegated to that populace with high certainty. Cases of populace task in measurable casework incorporate Wasser et al. (2007, 2008) (9, 10) where they set up the geographic beginning of elephant tusks and hankos from one of the biggest ivory seizures ever made. After at first making an expansive database of allelic frequencies at least seven STR loci from more than 500 reference tests of known starting point over the dispersion scope of backwoods and savannah elephants in Africa, Wasser et al. (2007, 2008) (9, 10) utilized the spatial smoothing technique executed in the product SCAT (http://stephenslab.uchicago.edu/software.html) to make a guide of allelic frequencies over a ceaseless range. This permitted them to assess allele frequencies even at areas which had not been tested (i.e. no allele recurrence information was straightforwardly accessible) and permitted populace task tests on tests from obscure areas. Although just an extent of tests were effectively enhanced at seven loci, their outcomes proposed that tusks (n = 37) were relegated to southern Africa, focused on Zambia while the hankos (n = 12) relegated somewhat upper east of Zambia. While it is conceivable that tusks from various inceptions were simply not effectively genotyped, these reviews highlight the convenience of such a study which permits preservation and law requirement push to be directed in particular regions. Bayesian techniques for task with no need for from the earlier assignment of populaces and permitting admixture are progressively being utilized. From the earlier assignment of populaces in light of data, for example, accumulation destinations or political limits with no admixture is thought prone to predisposition task comes about furthermore, is probably not going to reflect genuine organic circumstances. The Bayesian technique and programming structure created by Pritchard et al. (2000) (90) furthermore, Falush et al. (2003) (91) can first gather the quantity of populaces from the information by augmenting Hardy Weinberg balance and limiting linkage disequilibrium inside bunches while permitting admixture, and after that accordingly appoint people to a group, making it a very well known strategy for populace task (23, 26-27, 37). Ball et al. (2011) (28) tried the "frequentist" (i.e. allele recurrence based) and the Bayesian "managed" (from the earlier populace task with no admixture) and "unsupervised" (no from the earlier populace task with admixture) approaches utilizing three criminological casework tests of moose. In light of the outcomes acquired, these creators additionally suggested receiving the Bayesian "unsupervised" approach.

7. CONCLUSION

The potential offered by DNA examination in legal examinations into creature mistreatment and biodiversity protection is patently clear from the different cases highlighted above, and given the scale furthermore, nature of the issue at present confronted with creature insurance furthermore, biodiversity protection, it is sure to stay fundamental. As for species distinguishing proof, in spite of the fact that NGS advances offer enormous guarantee in expanding arrangement data and throughput of tests, aggregation of satisfactory reference information to permit measurable utilization crosswise over numerous species is impossible for a few a long time to come. Until that time, species recognizable proof will fundamentally depend on existing DNA bar-coding strategy with its natural issues. In any case, it is conceivable to a degree to relieve a number of these issues. Firstly, it is plentifully certain that ordered scope and inspecting inside taxa should be essentially enhanced inside BOLD to enhance unwavering quality of species identification. Secondly, when investigating groupings for species recognizable proof, it is imperative to experimentally test different models of development as opposed to receive the K2P separate model as standard. At long last, upgrading particular preliminaries instead of depending on general groundworks can help diminish a portion of the issues related with heteroplasmy, co-amplification of numts, and absence of reliable intensification crosswise over taxa. With regard to individualisation and populace task, both are achievable with abnormal amounts of likelihood utilizing STRs. Regardless of the way that NGS advances will bring about the distinguishing proof of extensive quantities of Single Nucleotide Polymorphisms (SNPs) in numerous species in coming years and that SNPs offer many points of interest to STRs (Ogden 2011), STRs are probably going to keep on being the marker of decision for quite a while sufficient reference information on SNPs is gathered.

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There is much arrangement and STR information officially accessible in numerous species from protection and populace genetics reviews yet this information is not promptly material to measurable casework. For instance, in most untamed life species (dissimilar to in human and some local domestic for example, felines and canines), there is a dominance of di-nucleotide STR markers in the writing which are not perfect for measurable science in view of falter items produced amid PCR which can make conclusive allele calling troublesome. Furthermore, in natural life species, STR markers created in one animal groups are regularly utilized as a part of other firmly related species because of saved PCR preliminary restricting locales e.g. reindeer markers in red, roe and neglected deer (92), bovid and ovid markers in mule deer (46). There are issues related with this cross-species intensification, including an expanded plausibility of invalid alleles and poor repeatability due to confuse in groundwork restricting districts. In this way, when legal application is required, not at all like in populace or preservation hereditary reviews, there is an unmistakable requirement for extra research into approval and quality affirmation via doing an earlier appraisal of unwavering quality of all phases of the procedure (93-94).

What is obviously required is more prominent collaboration between protection geneticists and criminological geneticists, something beforehand likewise worried by others (94-95). This will bring about a more prominent familiarity with criminological viewpoints among preservation geneticists and of protection hereditary perspectives among legal geneticists. Salas et al. (2005, 2007) (96-97) displayed confirm for problematic use of human mt DNA information by legal geneticists and lamented the way that scientific geneticists were uninformed of transformative hereditary wording and phylogenetic examinations. Consequently, enhanced forensic information in protection geneticists and enhanced transformative addition to this, phylogenetic learning in scientific geneticists won't just permit preservation hereditary qualities tasks to illuminate protection as proposed, however will likewise all the while give DNA devices and fundamental data on populace structure and developmental history of an animal groups for criminological geneticists to all the more adequately and dependably apply DNA examinations in scientific examinations. Forensic research facilities are generally certify to global guidelines with a specific end goal to show the elevated amounts of capability required when proof is to be exhibited in a court of law. Few wild life legal sciences research facilities will be that as it may, have the capacity to bear the cost of the high expenses related with this accreditation procedure, and an absence of accreditation may bring about proof being tested in court. There is presently a sensible other option to both these difficulties. The Scientific Working Group for Wildlife Forensic Sciences (SWGWILD) of the Society for Wildlife Forensic Science (SWFS) has as of late ordered a far reaching set of norms and rules for experts of untamed life scientific science (98), and offers a capability testing and accreditation program for an ostensible expense where people can apply for affirmation as an untamed life scientific researcher.

REFERENCES

1. Iyengar Arati. (2014). Forensic DNA analysis for animal protection and biodiversity conservation: A review. Journal for Nature Conservation 22 : 195–205.
2. IUCN. (2013). The IUCN Red list of threatened species. Version 2013.1. Available athttp://www.iucnredlist.org (accessed 27.10.13).
3. Fang, S., & Wan, Q. (2003). A genetic fingerprinting test for identifying carcasses of protected deer species in China. Biological Conservation, 103, 371–373.
4. Gupta, S. K., Verma, S. K., & Singh, L. (2005). Molecular insight into a wildlife crime: The case of a peafowl slaughter. Forensic Science International, 154, 214–217.
5. Wu, H., Wan, Q.-H., Fang, S.-G., & Zhang, S.-Y. (2005). Application of mitochon-drial DNA sequence analysis in the forensic identification of Chinese sika deer subspecies. Forensic Science International, 148, 101–105.
6. Lorenzini, R. (2005). DNA forensics and the poaching of wildlife in Italy: A case study. Forensic Science International, 153, 218–221.
7. Shivji, M. S., Chapman, D. D., Pikitch, E. K., & Raymond, P. W. (2005). Genetic profiling reveals illegal international trade in fins of the great white shark Carcharodoncarcharias. Conservation Genetics, 6(6), 1035–1039.
8. An, J., Lee, M.-Y., Min, M.-S., Lee, M.-H., & Lee, H. (2007). A molecular genetic approach for species identification of mammals and sex determination of birds in a foren-sic case of poaching from South Korea. Forensic Science International, 167, 59–61.
9. Wasser, S. K., Mailand, C., Booth, R., Mutayoba, B., Kisamo, E., Clark, B., et al. (2007).Using DNA to track the origin of the largest ivory seizure since the 1989 tradeban. Proceedings of the National Academy of Sciences of the United States of America,104(10), 4228–4233.
10. Wasser, S. K., Clark, W. J., Drori, O., Kisamo, E. S., Mailand, C., Mutayoba, B., et al.(2008). Combating the illegal trade in African elephant ivory with DNA forensics. Conservation Biology, 22(4), 1065–1071.
11. Linacre, A., & Tobe, S. S. (2008). On the trial of tigers – Tracking tiger in traditional East Asian Medicine. Forensic Science International: Genetics, 1, 603–604.
12. Dalebout, M. L., Robertson, K. M., Chivers, S. J., & Samuels, A. (2008). DNA identification and the impact of illegal,

unregulated, and unreported (IUU) fishing on rare whales in Micronesian waters. Micronesica, 40(1/2), 139–147.
13. Peppin, L., McEwing, R., Carvalho, G. R., & Ogden, R. (2008). A DNA-based approach forthe forensic identification of Asiatic black bear (Ursus thibetanus) in a traditional Asian medicine. Journal of Forensic Sciences, 53(6), 1358–1362.
14. Fumagalli, L., Cabrita, C. J., & Castella, V. (2009). Simultaneous identification of multiple mammalian species from mixed forensic samples based on mtDNA control region length polymorphism. Forensic Science International: Genetics Supplement Series, 2, 302–303.
15. Martin, J. C., Saucedo, C. E., Corti, P., & González, B. A. (2009). Application of DNA forensic techniques for identifying poached guanacos (Lama guanicoe) in ChileanPatagonia. Journal of Forensic Sciences, 54(5), 1073–1076.
16. Eiken, H. G., Andreassen, R. J., Kopatz, A., Bjervamoen, S. G., Wartianen, I., Tobiassen,C., et al. (2009). Population data for 12 STR loci in Northern European brown bear(Ursus arctos) and application of DNA profiles for forensic casework. Forensic Science International: Genetics Supplement Series, 2, 273–274.
17. Baker, C. S., Steel, D., Choi, Y., Lee, H., Kim, K. S., Choi, S. K., et al. (2010). Genetic evidence of illegal trade in protected whales links Japan with the US and SouthKorea. Biology Letters, http://dx.doi.org/10.1098/rsbl.2010.0239.
18. Filonzi, L., Chiesa, S., Vaghi, M., & Marzano, F. N. (2010). Molecular barcoding reveals mislabeling of commercial fish products in Italy. Food Research International, 43,1383–1388.
19. Eaton, M. J., Meyers, G. L., Kolokotronis, S.-O., Leslie, M. S., Martin, A. P., & Amato,G. (2010). Barcoding bush meat: Molecular identification of Central African and South American harvested vertebrates. Conservation Genetics, 11, 1389–1404.
20. Ghobrial, L., Lankester, F., Kiyang, J. A., Akih, A. E., de Vries, S., Fotso, R., et al. (2010).Tracing the origins of rescued chimpanzees reveals widespread chimpanzee hunting in Cameroon. BMC Ecology, 10, 2.
21. Caniglia, R., Fabbri, E., Greco, C., Galaverni, M., & Randi, E. (2010). Forensic DNA against wildlife poaching: Identification of a serial wolf killing in Italy. Forensic Science International: Genetics, 4, 334–338.
22. Gupta, S. K., Thangaraj, K., & Singh, L. (2011). Case report. Identification of the source of ivory idol by DNA analysis. Journal of Forensic Sciences, 56(5), 1343–1345.
23. Lorenzini, R., Cabras, P., Fanelli, R., & Carboni, G. L. (2011). Wildlife molecular forensics: Identification of the Sardinian mouflon using STR profiling and the Bayesian assignment test. Forensic Science International: Genetics, 5, 345–349.
24. Coghlan, M. L., White, N. E., Parkinson, L., Haile, J., Spencer, P. B. S., & Bunce, M.(2011). Egg forensics: An appraisal of DNA sequencing to assist in species identification of illegally smuggled eggs. Forensic Science International: Genetics, 6(2),268–273.
25. Dalton, D. L., & Kotze, A. (2011). DNA barcoding as a tool for species identification in three forensic wildlife cases in South Africa. Forensic Science International, 207,e51–e54.
26. Alasaad, S., Schuster, R. K., Gakuya, F., Theneyan, M., Jowers, M. J., Maione, S., et al.(2011). Applicability of molecular markers to determine parasitic infection ori-gins in the animal trade: A case study from Sarcoptes mites in wildebeest. Forensic Science, Medicine, & Pathology, 8(3), 280–284.
27. Di Rocco, F., Posik, D. M., Ripoli, M. V., Díaz, S., Maté, M. L., Giovambattista, G., et al.(2011). South American camelid illegal traffic detection by means of molecularmarkers. Legal Medicine, 13, 289–292.
28. Ball, M. C., Finnegan, L. A., Nette, T., Broders, H. G., & Wilson, P. J. (2011). Wildlife forensics: "Supervised" assignment testing can complicate the association of suspect cases to source populations. Forensic Science International: Genetics, 5,50–56.
29. Sanches, A., Perez, W. A. M., Figueiredo, M. G., Rossini, B. C., Cervini, M., Galetti, P.M., Jr., et al. (2011). Wildlife forensic DNA and lowland tapir (Tapirus terrestris)poaching. Conservation Genetic Resources, 3, 189–193.
30. Jun, J., Han, S. H., Jeong, T.-J., Park, Y. C., Lee, B., & Kwak, M. (2011). Wildlife forensics using mitochondrial DNA sequences: Species identification based on hairs collected in the field and confiscated tanned Felidae leathers. Genes and Genomics,33, 721–726.
31. Wesselink, M., & Kuiper, I. (2011). Individual identification of fox (Vulpes vulpes) in forensic wildlife investigations. Forensic Science International: Genetics Supplement Series, 3, e214–e215.
32. Gaur, A., Singh, C. S., Sreenivas, A., & Singh, L. (2012). Letter to the editor. DNA-based identification of a snake in a wine bottle using universal primers: A case of mistaken identity. Forensic Science International, 214, e51–e53.
33. White, N. E., Dawson, R., Coghlan, M. L., Tridico, S. R., Mawson, P. R., Haile, J., et al.(2012). Case report. Application of STR markers in wildlife forensic casework involving Australian black-cockatoos (Calyptorhynchus spp.). Forensic Science International: Genetics, 6, 664–670.
34. Barbanera, F., Guerrini, M., Beccani, C., Forcina, G., Anayiotos, P., & Panayides, P.(2012). Case report. Conservation of endemic and threatened wildlife: Molecular forensic DNA against poaching of the Cypriot mouflon (Ovis orientalis

ophion, Bovidae). Forensic Science International: Genetics, 6, 671–675.
35. Abe, H., Hayano, A., & Inoue-Murayama, M. (2012). Forensic species identification of large macaws using DNA barcodes and microsatellite profiles. Molecular Biology Reports, 39, 693–699.
36. Doukakis, P., Pikitch, E. K., Rothschild, A., DeSalle, R., Amato, G., & Kolokotronis, S.-O.(2012). Testing the effectiveness of an international conservation agreement: Marketplace forensics and CITES caviar trade regulation. PLoS One, 7(7), e40907.http://dx.doi.org/10.1371/journal.pone.0040907.
37. Caniglia, R., Fabbri, E., Mastrogiuseppe, L., & Randi, E. (2013). Case report. Who is who? Identification of livestock predators using forensic genetics approaches.Forensic Science International: Genetics, 7, 397–404.
38. Lee, E.-J., Lee, Y.-H., Moon, S.-H., Kim, N.-Y., Kim, S.-H., Yang, M.-S., et al. (2013).Case report. The identification of elephant ivory evidences of illegal trade with mitochondrial cytochrome b gene and hyper variable D-loop region. Journal of Forensic and Legal Medicine, 20, 174–178.
39. Welton, L. J., Siler, C. D., Linkem, C. W., Diesmos, A. C., Diesmos, M. L., Sy, E., et al.(2013). Dragons in our midst: Phyloforensics of illegally traded Southeast Asianmonitor lizards. Biological Conservation, 159, 7–15.
40. Hsieh, H.-M., Huang, L.-H., Tsai, L.-C., Kuo, Y.-C., Meng, H.-H., Linacre, A., et al. (2003).Species identification of rhinoceros horns using the cytochrome b gene. Forensic Science International, 136, 1–11.
41. Xu, Y. C., Li, B., Li, W. S., Bai, S. Y., Jin, Y., Li, X. P., et al. (2005). Individualization of tiger by using microsatellites. Forensic Science International, 151, 45–51.
42. Yan, P., Wu, X.-B., Shi, Y., Gu, C.-M., Wang, R.-P., & Wang, C.-L. (2005). Identification of Chinese alligators (Alligator sinensis) meat by diagnostic PCR of the mitochondrial cytochrome b gene. Biological Conservation, 121, 45–55.
43. Clarke, S. C., Magnussen, J. E., Abercrombie, D. L., McAllister, M. K., & Shivji, M. S.(2006). Identification of shark species composition and proportion in the HongKong shark fin market based on molecular genetics and trade records. Conservation Biology, 20, 201–211.
44. Lee, J. C.-I., Tsai, L.-C., Yang, C.-Y., Liu, C.-L., Huang, L.-H., Linacre, A., et al. (2006).DNA profiling of Shahtoosh. Electrophoresis, 27(17), 3359–3362.
45. Baker, C. S., Cooke, J. G., Lavery, S., Dalebout, M. L., Yu, M., Funashi, N., et al.(2007). Estimating the number of whales entering trade using DNA profil-ing and capture–recapture analysis of market products. Molecular Ecology, 16, 2617–2626.
46. Jobin, R. M., Patterson, D., & Zhang, Y. (2008). DNA typing in populations of muledeer for forensic use in the Province of Alberta. Forensic Science International: Genetics, 2, 190–197.
47. Sanders, J. G., Cribbs, J. E., Fienberg, H. G., Hulburd, G. C., Katz, L. S., & Palumbi, S.R. (2008). The tip of the tail: Molecular identification of seahorses for sale in apothecary shops and curio stores in California. Conservation Genetics, 9, 65–71.
48. Szabolsci, Z., Egyed, B., Zenke, P., Borsy, A., Pádár, Z., Zöldág, L., et al. (2008). Genetic identification of red deer using autosomal STR markers. Forensic Science Inter-national: Genetics Supplement Series, 1, 623–624.
49. Lee, J. C.-I., Tsai, L.-C., Liao, S.-P., Linacre, A., & Hsieh, H.-M. (2009). Species identifi-cation using the cytochrome b gene of commercial turtle shells. Forensic Science International: Genetics, 3, 67–73.
50. Meganathan, P. R., Dubey, B., Jogayya, K. N., & Haque, I. (2011). Validation of a mul-tiplex PCR assay for the forensic identification of Indian crocodiles. Journal of Forensic Sciences, 56(5), 1241–1244.
51. Kress, W. J., Wurdack, K. J., Zimmer, E. A., Welgt, L. A., & Janzen, D. H. (2005). Use of DNA barcodes to identify flowering plants. Proceedings of the National Academy of Sciences of the United States of America, 102(23), 8369–8374.
52. Ogden, R., McGough, H. N., Cowan, R. S., Chua, L., Groves, M., & McEwing, R. (2008).SNP-based method for the genetic identification of ramin Gonystylus spp. timber and products: Applied research meeting CITES enforcement needs. Endangered Species Research, http://dx.doi.org/10.3354/esr00141.
53. Tnah, L. H., Lee, S. L., Ng, K. K. S., Tani, N., Bhassu, S., & Othman, R. Y. (2009). Geographical traceability of an important tropical timber (Neobalanocarpus heimii) inferred from chloroplast DNA. Forest Ecology and Management, 258, 1918–1923.
54. Tnah, L. H., Lee, S. L., Ng, K. K. S., Faridah, Q.-Z., & Faridah-Hanum, I. (2010). Forensic DNA profiling of tropical timber species in peninsular Malaysia. Forest Ecology and Management, 259, 1436–1446.
55. Eurlings, M. C. M., van Beek, H. H., & Gravendeel, B. (2010). Polymorphic microsatellite for forensic identification of agar wood (Aquilaria crassna). Forensic Science International, 197, 30–34.
56. Jolivet, C., & Degen, B. (2012). Use of DNA fingerprints to control the origin of sapelli timber (Entandrophragma cylindricum) at the forest concession level in Cameroon. Forensic Science International: Genetics, 6, 487–493.

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Species, 2017, 18(59), 77-90,

57. Pinhal, D., Shivji, M. S., Nachtigall, P. G., Chapman, D. D., & Martins, C.(2012). A streamlined DNA tool for global identification of heavily exploited coastal shark species (Genus Rhizoprionodon). PLoS ONE, 7(4), e34797. http://dx.doi.org/10.1371/journal.pone.0034797.
58. Ratnasingham, S., & Hebert, P. D. N. (2007). BOLD: The barcode of life data system.(www.barcodinglife.org), Molecular Ecology Notes, 7, 355–364.
59. Hebert, P. D. N., Stoeckle, M. Y., Zemlak, T. S., & Francis, C. M. (2004).Identification of birds through DNA barcodes. PLoS Biology, 2(10), e312.http://dx.doi.org/10.1371/journal.pbio.0020312.
60. Ivanova, N. V., Zemlak, T. S., Hanner, R. H., & Hebert, P. D. N. (2007). Universal primer cocktails for fish DNA barcoding. Molecular Ecology Notes, 7(4), 544–548.
61. Naro-Maciel, E., Reid, B., Fitzsimmons, N. N., Le, M., Desalle, R., & Amato, G. (2010).DNA barcodes for globally threatened marine turtles: A registry approach to documenting biodiversity. Molecular Ecology Resources, 10, 252–263.
62. Bitanyi, S., Bjørnstad, G., Ernest, E. M., Nesie, M., Kusiluka, L. J., Keyyu, J. D., et al.(2011). Species identification of Tanzanian antelopes using DNA barcoding. Molecular Ecology Resources, 11(3), 442–449.
63. Clare, E. L., Lim, B. K., Fenton, M. B., & Hebert, P. D. N. (2011). Neotropical bats: Estimating species diversity with DNA barcodes. PLoS ONE, 6(7), e22648.
64. Galtier, N., Nabholz, B., Glémin, S., & Hurst, G. D. D. (2009). Mitochondrial DNA as a marker of molecular diversity: A reappraisal. Molecular Ecology, 18, 4541–4550.
65. Vences, M., Thomas, M., Bonett, R. M., & Vieites, D. R. (2005). Deciphering amphibian diversity through DNA barcoding: Chances and challenges. Philosophical Trans-actions of the Royal Society B: Biological Sciences, 360, 1859–1868.
66. Hebert, P. D. N., Cywinska, A., Ball, S. L., & deWaard, J. R. (2003). Biological identifications through DNA barcodes. Proceedings of the Royal Society of London SeriesB, 270, 313–321.
67. Srivathsan, A., & Meier, R. (2012). On the inappropriate use of Kimura-2-parameter (K2P) divergences in the DNA-barcoding literature. Cladistics, 28, 190–194.
68. Boykin, L. M., Armstrong, K., Kubatko, L., & De Barro, P. (2012). DNA barcoding invasive insects: database roadblocks. Invertebrate Systematics, 26, 506–514.
69. Coghlan, M. L., White, N. E., Parkinson, L., Haile, J., Spencer, P. B. S., & Bunce, M.(2011). Egg forensics: An appraisal of DNA sequencing to assist in species identification of illegally smuggled eggs. Forensic Science International: Genetics, 6(2),268–273.
70. Taylor, H. R., & Harris, W. E. (2012). An emergent science on the brink of irrelevance: A review of the past 8 years of DNA barcoding. Molecular Ecology Resources, 12,377–388.
71. Wilson-Wilde, L., Norman, J., Robertson, J., Sarre, S., & Georges, A. (2010). Current issues in species identification for forensic science and the validity of using thecytochrome oxidase I (COI) gene. Forensic Science, Medicine and Pathology, 6,233–241.
72. Hollingsworth, P. M., Graham, S. W., & Little, D. P. (2011). Choosing and using a plant DNA barcode. PLoS One, 6(5), e19254.http://dx.doi.org/10.1371/journal.pone.0019254.
73. Magnacca, K. N., & Brown, M. J. F. (2010). Mitochondrial heteroplasmy and DNA barcoding in Hawaiian Hylaeus (Nesoprosopis) bees (Hymenoptera: Colletidae).BMC Evolutionary Biology, 10, 174.
74. Lopez, J. V., Yuhki, N., Masuda, R., Modi, W., & O'Brien, S. J. (1994). Numt, a recent transfer and tandem amplification of mitochondrial DNA to the nuclear genome of the domestic cat. Journal of Molecular Evolution, 39, 174–190.
75. Moulton, M. J., Song, H., & Whiting, M. F. (2010). Assessing the effects of primer specificity on eliminating numt co-amplification in DNA barcoding: A case study from Orthoptera (Arthropoda: Insecta). Molecular Ecology Resources, 10, 615–627.
76. Richly, E., & Leister, D. (2004). NUMTs in sequenced eukaryotic genomes. Molecular Biology and Evolution, 21, 1081–1084.
77. De Salle, R., Egan, M. G., & Siddall, M. (2005). The unholy trinity: taxonomy, species delimitation and DNA barcoding. Philosophical transactions of the Royal Society B, 360, 1905–1916.
78. Wasser, S. K., Shedlock, A. M., Comstock, K., Ostrander, E. A., Mutayoba, B., & Stephens,M. (2004). Assigning African elephant DNA to geographic region of origin: Appli-cations to the ivory trade. Proceedings of the National Academy of Sciences of the United States of America, 101(41), 14847–14852.
79. Dawnay, N., Ogden, R., Thorpe, R. S., Pope, L. C., Dawson, D. A., & McEwing, R. (2008). A forensic STR profiling system for the Eurasian badger: A framework for develop-ing profiling systems for wildlife species. Forensic Science International: Genetics,2, 47–53.
80. Dawnay, N., Ogden, R., Wetton, J. H., Thorpe, R. S., & McEwing, R. (2009). Genetic datafrom 28 STR loci for forensic individual identification and parentage analyses in6 bird of prey species. Forensic Science International: Genetics, 3, e63–e69.
81. Caratti, S., Rossi, L., Sona, B., Origlia, S., Viara, S., Martano, G., et al. (2010). Analy-sis of 11 tetrameric STRs in wild boars for

forensic purposes. Forensic Science International Genetics, 4, 339–342.
82. Harper, C. K., Vermeulen, G. J., Clarke, A. B., de Wet, J. I., & Guthrie, A. J. (2013).Extraction of nuclear DNA from rhinoceros horn and characterization of DNA profiling systems for white (Ceratotherium simum) and black (Diceros bicornis)rhinoceros. Forensic Science International: Genetics, 7, 428–433.
83. Schneider, P. M. (2007). Scientific standards for studies in forensic genetics. Forensic Science International, 165, 238–243.
84. Andreassen, R., Schregel, J., Kopatz, A., Knappskog, P. M., Hagen, S. B., Kleven, O.,et al. (2012). A forensic DNA profiling system for Northern European brown bears (Ursus arctos). Forensic Science International: Genetics, 6, 798–809.
85. Barton, N. H., Briggs, D. E. G., Eisen, J. A., Goldstein, D. P., & Patel, N. H. (2007).Evolution. New York, USA: Cold Spring Harbor Laboratory Press.
86. Budowle, B., Shea, B., Niezgoda, S., & Chakraborty, R. (2001). CODIS STR loci data from 41 sample populations. Journal of Forensic Sciences, 46(3), 453–489.
87. Ayres, K. L., & Overall, A. D. (1999). Allowing for within-subpopulation inbreeding in forensic match probabilities. Forensic Science International, 103, 207–216.
88. Waits, L. P., Luikart, G., & Taberlet, P. (2001). Estimating the probability of identity among genotypes in natural populations: Cautions and guidelines. Molecular Ecology, 10, 249–256.
89. Wesselink, M., & Kuiper, I. (2011). Individual identification of fox (Vulpes vulpes) in forensic wildlife investigations. Forensic Science International: Genetics Supplement Series, 3, e214–e215.
90. Pritchard, J. K., Stephens, M., & Donnelly, P. (2000). Inference of population structure using multilocus genotype data. Genetics, 155, 945–959.
91. Ogden, R. (2011). SNP discovery: Next generation sequencing, unlocking the potential of genomic technologies for wildlife forensics. Molecular Ecology Resources, 11(Suppl. 1), 109–116.
92. Poetsch, M., Seefeldt, S., Maschke, M., & Lignitz, E. (2001). Analysis of microsatellite polymorphism in red deer, roe deer, and fallow deer – Possible employment in forensic applications. Forensic Science International, 116, 1–8.
93. Linacre, A., Gusmaõ, L., Hecht, W., Hellmann, A. P., Mayr, W. R., Parson, W., et al.(2011). ISFG: Recommendations regarding the use of non-human (animal) DNA in forensic genetic investigations. Forensic Science International: Genetics, 5(5), 501–505.
94. Ogden, R., Dawnay, N., & McEwing, R. (2009). Wildlife DNA forensics – Bridging the gap between conservation genetics and law enforcement. Endangered Species Research, 9, 179–195.
95. Alacs, E. A., Georges, A., FitzSimmons, N. N., & Robertson, J. (2010). DNA detective: A review of molecular approaches to wildlife forensics. Forensic Science, Medicineand Pathology, 6, 180–194.
96. Salas, A., Carracedo, A., Macauley, V., Richards, M., & Bandelt, H.-J. (2005). A practical guide to mitochondrial DNA error prevention in clinical, forensic and population genetics. Biochemical and Biophysical Research Communications, 335, 891–899.
97. Salas, A., Bandelt, H.-J., Macauley, V., & Richards, M. B. (2007). Phylogeographic investigations: The role of trees in forensic genetics. Forensic Science International, 168, 1–13.
98. SWGWILD. (2013). SWGWILD standards and guidelines (Version 2.0 – Accepted by SWGWILD December 19, 2012). Available at http://www.wildlifeforensicscience.org/swgwild/ (accessed 07.11.13)